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## RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/082,902

TIME: 10:01:08

Input Set : N:\Cr3\RULE60\10082902.raw

Output Set: N:\CRF3\04112002\J082902.raw

1 <110> APPLICANT: Ballinger, Dennis G.  
 2 Montgomery, Julie R.  
 3 <120> TITLE OF INVENTION: Growth Factor Antagonist Materials and Methods  
 4 <130> FILE REFERENCE: 28110/35878  
 5 <140> CURRENT APPLICATION NUMBER: 10/082,902  
 6 <141> CURRENT FILING DATE: 2002-02-26  
 9 <150> PRIOR APPLICATION NUMBER: US/09/370,398  
 10 <151> PRIOR FILING DATE: 1998-08-06  
 13 <160> NUMBER OF SEQ ID NOS: 13  
 14 <170> SOFTWARE: PatentIn Ver. 2.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1662  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Homo sapiens  
 20 <220> FEATURE:  
 21 <221> NAME/KEY: CDS  
 22 <222> LOCATION: (211)..(1107)  
 23 <400> SEQUENCE: 1  
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 25 gttcctccga ccggcgtctg cgagtacagc ggcggctaac ctgccccggc ttcaggattt 120  
 26 acacagacgt ggggcgatgc ttgtgacct gcagctcctc aaaggccctt agaagcctgt 180  
 27 ttctccgtac agtccaggac ctccagcccc atg gag ccc ccg atc cca gag agc 234  
 28 Met Glu Pro Pro Ile Pro Gln Ser  
 29 1 5  
 30 gcc ccc ttg act ccc aac tca gtc atg gtc cag ccc ctt ctt gac agc 282  
 31 Ala Pro Leu Thr Pro Asn Ser Val Met Val Gln Pro Leu Leu Asp Ser  
 32 10 15 20  
 33 cgg atg tcc cac agc cgg ctc cag cac cca ctc acc atc cta ccc att 330  
 34 Arg Met Ser His Ser Arg Leu Gln His Pro Leu Thr Ile Leu Pro Ile  
 35 25 30 35 40  
 36 gac cag gtg aag acc agc cat gtg gag aat gac tac ata gac aac cct 378  
 37 Asp Gln Val Lys Thr Ser His Val Glu Asn Asp Tyr Ile Asp Asn Pro  
 38 45 50 55  
 39 agc ctg gcc ctg acc acc ggc cca aag cgg acc cgg ggc ggg gcc cca 426  
 40 Ser Leu Ala Leu Thr Thr Gly Pro Lys Arg Thr Arg Gly Gly Ala Pro  
 41 60 65 70  
 42 gag ctg gcc ccg acg ccc gcc cgc tgt gac cag gat gtc acc cac cat 474  
 43 Glu Leu Ala Pro Thr Pro Ala Arg Cys Asp Gln Asp Val Thr His His  
 44 75 80 85  
 45 tgg atc tcc ttc agc ggg cgc ccc agc tct gtg agc agc agc agc agc 522  
 46 Trp Ile Ser Phe Ser Gly Arg Pro Ser Ser Val Ser Ser Ser Ser Ser  
 47 90 95 100  
 48 aca tcc tct gac caa cgg ctc tta gac cac atg gca cca cca ccc gtg 570

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49   Thr Ser Ser Asp Gln Arg Leu Leu Asp His Met Ala Pro Pro Pro Val
50   105                               110                               115                               120
51   gct gac cag gcc tca cca agg gct gtg cgc atc cag ccc aag gtg gtc      618
52   Ala Asp Gln Ala Ser Pro Arg Ala Val Arg Ile Gln Pro Lys Val Val
53   125                               130                               135
54   cac tgc cag ccg ctg gac ctc aag ggc ccg gcg gtc cca ccc gag ctg      666
55   His Cys Gln Pro Leu Asp Leu Lys Gly Pro Ala Val Pro Pro Glu Leu
56   140                               145                               150
57   gac aag cac ttc ttg ctg tgc gag gcc tgt ggg aag tgt aaa tgc aag      714
58   Asp Lys His Phe Leu Leu Cys Glu Ala Cys Gly Lys Cys Lys Cys Lys
59   155                               160                               165
60   gag tgt gca tcc ccc cgg acg ttg cct tcc tgc tgg gtc tgc aac cag      762
61   Glu Cys Ala Ser Pro Arg Thr Leu Pro Ser Cys Trp Val Cys Asn Gln
62   170                               175                               180
63   gag tgc ctg tgc tca gcc cag act ctg gtc aac tat ggc acg tgc atg      810
64   Glu Cys Leu Cys Ser Ala Gln Thr Leu Val Asn Tyr Gly Thr Cys Met
65   185                               190                               195                               200
66   tgt ttg gtg cag ggc atc ttc tac cac tgc acg aat gag gac gat gag      858
67   Cys Leu Val Gln Gly Ile Phe Tyr His Cys Thr Asn Glu Asp Asp Glu
68   205                               210                               215
69   ggc tcc tgc gct gac cac ccc tgc tcc tgc tcc cgc tcc aac tgc tgc      906
70   Gly Ser Cys Ala Asp His Pro Cys Ser Cys Ser Arg Ser Asn Cys Cys
71   220                               225                               230
72   gcc cgc tgg tcc ttc atg ggt gct ctc tcc gtg gtg ctg ccc tgc ctg      954
73   Ala Arg Trp Ser Phe Met Gly Ala Leu Ser Val Val Leu Pro Cys Leu
74   235                               240                               245
75   ctc tgc tac ctg cct gcc acc ggc tgc gtg aag ctg gcc cag cgt ggc      1002
76   Leu Cys Tyr Leu Pro Ala Thr Gly Cys Val Lys Leu Ala Gln Arg Gly
77   250                               255                               260
78   tac gac cgt ctg cgc cgc cct ggt tgc cgc tgc aag cac acg aac agc      1050
79   Tyr Asp Arg Leu Arg Arg Pro Gly Cys Arg Cys Lys His Thr Asn Ser
80   265                               270                               275                               280
81   gtc atc tgc aaa gca gcc agc ggg gat gcc aag acc agc agg ccc gac      1098
82   Val Ile Cys Lys Ala Ala Ser Gly Asp Ala Lys Thr Ser Arg Pro Asp
83   285                               290                               295
84   aag cct ttc tgacagtttg tgtcgaagcc ccagtgcctc gcctggaaac      1147
85   Lys Pro Phe
87   ctggtttctc tctgacatct aagaagactg cagcaaggtc agaggtttta gcctcctgag 1207
88   gctgaccttg ctagtctgcc cactccctac cccagcttc ggaaaataca gagaccacca 1267
89   ccacgtaccc tgtattcccc aagatgatga agaagcactt tggggctttt ttccagggtc 1327
90   ctgaaacttt gtgtcaaaca gacaatgcag gggcagggtg tggtttgggg ggaaattttt 1387
91   ctttttcaga agacagaaca cagatgtgga cacatatccg gaaactgcag ctgcttgaat 1447
92   gccttcccag cccctccttc tccctccctc cctccgcccc ccccttcctc ttttccattg 1507
93   tctttggcac tcacaggagc tagctgcctg ggaggaattg ctaactgagt accagggtac 1567
94   ctttaaagaa gacccttgga gtcttctata ccttcttctc cttccccatc tcactccacc 1627
95   ccactttgtc cctgatgtct tggggaaggt gtaga      1662
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 299
99 <212> TYPE: PRT

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100 &lt;213&gt; ORGANISM: Homo sapiens

101 &lt;400&gt; SEQUENCE: 2

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102   Met Glu Pro Pro Ile Pro Gln Ser Ala Pro Leu Thr Pro Asn Ser Val
103       1           5           10           15
104   Met Val Gln Pro Leu Leu Asp Ser Arg Met Ser His Ser Arg Leu Gln
105           20           25           30
106   His Pro Leu Thr Ile Leu Pro Ile Asp Gln Val Lys Thr Ser His Val
107           35           40           45
108   Glu Asn Asp Tyr Ile Asp Asn Pro Ser Leu Ala Leu Thr Thr Gly Pro
109           50           55           60
110   Lys Arg Thr Arg Gly Gly Ala Pro Glu Leu Ala Pro Thr Pro Ala Arg
111           65           70           75           80
112   Cys Asp Gln Asp Val Thr His His Trp Ile Ser Phe Ser Gly Arg Pro
113           85           90           95
114   Ser Ser Val Ser Ser Ser Ser Ser Thr Ser Ser Asp Gln Arg Leu Leu
115           100          105          110
116   Asp His Met Ala Pro Pro Pro Val Ala Asp Gln Ala Ser Pro Arg Ala
117           115          120          125
118   Val Arg Ile Gln Pro Lys Val Val His Cys Gln Pro Leu Asp Leu Lys
119           130          135          140
120   Gly Pro Ala Val Pro Pro Glu Leu Asp Lys His Phe Leu Leu Cys Glu
121           145          150          155          160
122   Ala Cys Gly Lys Cys Lys Cys Lys Glu Cys Ala Ser Pro Arg Thr Leu
123           165          170          175
124   Pro Ser Cys Trp Val Cys Asn Gln Glu Cys Leu Cys Ser Ala Gln Thr
125           180          185          190
126   Leu Val Asn Tyr Gly Thr Cys Met Cys Leu Val Gln Gly Ile Phe Tyr
127           195          200          205
128   His Cys Thr Asn Glu Asp Asp Glu Gly Ser Cys Ala Asp His Pro Cys
129           210          215          220
130   Ser Cys Ser Arg Ser Asn Cys Cys Ala Arg Trp Ser Phe Met Gly Ala
131           225          230          235          240
132   Leu Ser Val Val Leu Pro Cys Leu Leu Cys Tyr Leu Pro Ala Thr Gly
133           245          250          255
134   Cys Val Lys Leu Ala Gln Arg Gly Tyr Asp Arg Leu Arg Arg Pro Gly
135           260          265          270
136   Cys Arg Cys Lys His Thr Asn Ser Val Ile Cys Lys Ala Ala Ser Gly
137           275          280          285
138   Asp Ala Lys Thr Ser Arg Pro Asp Lys Pro Phe
139           290          295

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141 &lt;210&gt; SEQ ID NO: 3

142 &lt;211&gt; LENGTH: 315

143 &lt;212&gt; TYPE: PRT

144 &lt;213&gt; ORGANISM: Homo sapiens

145 &lt;400&gt; SEQUENCE: 3

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146   Met Glu Ala Arg Ala Gln Ser Gly Asn Gly Ser Gln Pro Leu Leu Gln
147       1           5           10           15
148   Thr Pro Arg Asp Gly Gly Arg Gln Arg Gly Glu Pro Asp Pro Arg Asp
149           20           25           30

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150   Ala Leu Thr Gln Gln Val His Val Leu Ser Leu Asp Gln Ile Arg Ala
151           35                     40                     45
152   Ile Arg Asn Thr Asn Glu Tyr Thr Glu Gly Pro Thr Val Val Pro Arg
153           50                     55                     60
154   Pro Gly Leu Lys Pro Ala Pro Arg Pro Ser Thr Gln His Lys His Glu
155           65                     70                     75                     80
156   Arg Leu His Gly Leu Pro Glu His Arg Gln Pro Pro Arg Leu Gln His
157           85                     90                     95
158   Ser Gln Val His Ser Ser Ala Arg Ala Pro Leu Ser Arg Ser Ile Ser
159           100                    105                    110
160   Thr Val Ser Ser Gly Ser Arg Ser Ser Thr Arg Thr Ser Thr Ser Ser
161           115                    120                    125
162   Ser Ser Ser Glu Gln Arg Leu Leu Gly Ser Ser Phe Ser Ser Gly Pro
163           130                    135                    140
164   Val Ala Asp Gly Ile Ile Arg Val Gln Pro Lys Ser Glu Leu Lys Pro
165           145                    150                    155                    160
166   Gly Glu Leu Lys Pro Leu Ser Lys Glu Asp Leu Gly Leu His Ala Tyr
167           165                    170                    175
168   Arg Cys Glu Asp Cys Gly Lys Cys Lys Cys Lys Glu Cys Thr Tyr Pro
169           180                    185                    190
170   Arg Pro Leu Pro Ser Asp Trp Ile Cys Asp Lys Gln Cys Leu Cys Ser
171           195                    200                    205
172   Ala Gln Asn Val Ile Asp Tyr Gly Thr Cys Val Cys Cys Val Lys Gly
173           210                    215                    220
174   Leu Phe Tyr His Cys Ser Asn Asp Asp Glu Asp Asn Cys Ala Asp Asn
175           225                    230                    235                    240
176   Pro Cys Ser Cys Ser Gln Ser His Cys Cys Thr Arg Trp Ser Ala Met
177           245                    250                    255
178   Gly Val Met Ser Leu Phe Leu Pro Cys Leu Trp Cys Tyr Leu Pro Ala
179           260                    265                    270
180   Lys Gly Cys Leu Lys Leu Cys Gln Gly Cys Tyr Asp Arg Val Asn Arg
181           275                    280                    285
182   Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Cys Cys Lys Val Pro
183           290                    295                    300
184   Thr Val Pro Pro Arg Asn Phe Glu Lys Pro Thr
185           305                    310                    315
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 139
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 4
192   Cys Glu Gln Cys Gly Lys Cys Lys Cys Gly Glu Cys Thr Ala Pro Arg
193           1                     5                     10                     15
194   Thr Leu Pro Ser Cys Leu Ala Cys Asn Arg Gln Cys Leu Cys Ser Ala
195           20                    25                    30
196   Glu Ser Met Val Glu Tyr Gly Thr Cys Met Cys Leu Val Lys Gly Ile
197           35                     40                     45
198   Phe Tyr His Cys Ser Asn Asp Asp Glu Gly Asp Ser Tyr Ser Asp Asn
199           50                     55                     60

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200   Pro Cys Ser Cys Ser Gln Ser His Cys Cys Ser Arg Tyr Leu Cys Met
201      65                      70                      75                      80
202   Gly Ala Met Ser Leu Phe Leu Pro Cys Leu Leu Cys Tyr Pro Pro Ala
203                      85                      90                      95
204   Lys Gly Cys Leu Lys Leu Cys Arg Arg Cys Tyr Asp Trp Ile His Arg
205                      100                    105                    110
206   Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Tyr Cys Lys Leu Glu
207                      115                    120                    125
208   Ser Cys Pro Ser Arg Gly Gln Gly Lys Pro Ser
209      130                      135
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 300
213 <212> TYPE: PRT
214 <213> ORGANISM: Mus musculus
215 <400> SEQUENCE: 5
216   Met Glu Pro Pro Val Pro Gln Ser Ser Val Pro Val Asn Pro Ser Ser
217      1                      5                      10                      15
218   Val Met Val Gln Pro Leu Leu Asp Ser Arg Ala Pro His Ser Arg Leu
219                      20                      25                      30
220   Gln His Pro Leu Thr Ile Leu Pro Ile Asp Gln Met Lys Thr Ser His
221                      35                      40                      45
222   Val Glu Asn Asp Tyr Ile Asp Asn Pro Ser Leu Ala Pro Ala Thr Gly
223      50                      55                      60
224   Pro Lys Arg Pro Arg Gly Gly Pro Pro Glu Leu Ala Pro Thr Pro Ala
225      65                      70                      75                      80
226   Arg Cys Asp Gln Asp Ile Thr His His Trp Ile Ser Phe Ser Gly Arg
227                      85                      90                      95
228   Pro Ser Ser Val Ser Ser Ser Ser Ser Thr Ser Ser Asp Gln Arg Leu
229                      100                    105                    110
230   Leu Asp His Met Ala Pro Pro Pro Val Ala Glu Gln Ala Ser Pro Arg
231                      115                    120                    125
232   Ala Val Arg Leu Gln Pro Lys Val Val His Cys Lys Pro Leu Asp Leu
233      130                      135                      140
234   Lys Gly Pro Thr Ala Pro Pro Glu Leu Asp Lys His Phe Leu Leu Cys
235      145                      150                    155                    160
236   Glu Ala Cys Gly Lys Cys Lys Cys Lys Glu Cys Ala Ser Pro Arg Thr
237                      165                    170                    175
238   Leu Pro Ser Cys Trp Val Cys Asn Gln Glu Cys Leu Cys Ser Ala Gln
239                      180                    185                    190
240   Thr Leu Val Asn Tyr Gly Thr Cys Met Cys Leu Val Gln Gly Ile Phe
241                      195                    200                    205
242   Tyr His Cys Thr Asn Glu Asp Asp Glu Gly Ser Cys Ala Asp His Pro
243      210                    215                    220
244   Cys Ser Cys Ser Gly Ser Asn Cys Cys Ala Arg Trp Ser Phe Met Gly
245      225                    230                    235                    240
246   Ala Leu Ser Val Val Leu Pro Cys Leu Leu Cys Tyr Leu Pro Ala Thr
247                      245                    250                    255
248   Gly Cys Val Lys Leu Ala Gln Arg Gly Tyr Asp Arg Leu Arg Arg Pro
249                      260                    265                    270

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/082,902

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